ESCAPE RNA Sequencing: Combining single cell protein and gene expression analysis

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Abstract
Recent advances in genomics technologies have made single cell gene expression analysis almost a routine workflow in biology today. However, gene expression analysis is only the latest tool available for studying single cell biology. Immunologists have studied single cell protein expression for 60 years. In an effort to combine decades worth of single cell protein expression data with the latest advances in genomics, we have developed the Enhanced Single Cell Analysis with Protein Expression (ESCAPE) platform. ESCAPE RNA sequencing provides researchers a way to confidently phenotype cells while still obtaining unbiased gene expression information. I will show the utility of these combination measurements in clinically relevant samples as well as provide early data looking at combining single cell protein expression with T cell receptor sequencing.

Recommended readings


Tuning up T-cell receptors. Rappazzo CG and Birnbaum ME. Nat Biotechnology 35 1145-1146 (2017).